

Method and Apparatus for Filtering and extending RNA alignment coverage

ABSTRACT

10 A technique is provided that is capable of extending a typically sparse RNA
alignment coverage, without creating redundant or improbable alignments. At
a high level, the invention provides a two-step process. The first step is to
combine and catenate all combinations of overlapping alignments that agree
with each other. The second step is to extend the boundaries of overlapping
15 alignments that agree with their first and last exons.